

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,630
Source: IFW0
Date Processed by STIC: 7/10/06

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IFWO

RAW SEQUENCE LISTING

DATE: 07/10/2006

PATENT APPLICATION: US/10/528,630

TIME: 09:46:22

Input Set : A:\BB-138.ST25.txt

Output Set: N:\CRF4\07102006\J528630.raw

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3 <110> APPLICANT: Bufe, Bernd
4   Hofmann, Thomas
5   Krautwurst, Dietmar
6   Kuhn, Christina
7   Meyerhof, Wolfgang
9 <120> TITLE OF INVENTION: Bitter taste receptors
11 <130> FILE REFERENCE: BB-138
13 <140> CURRENT APPLICATION NUMBER: US 10/528630
14 <141> CURRENT FILING DATE: 2005-03-22
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010691
17 <151> PRIOR FILING DATE: 2003-09-25
19 <150> PRIOR APPLICATION NUMBER: US 60/413298
20 <151> PRIOR FILING DATE: 2002-09-25
22 <160> NUMBER OF SEQ ID NOS: 52
24 <170> SOFTWARE: PatentIn version 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 333
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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38 20 25 30
41 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
42 35 40 45
45 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
46 50 55 60
49 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
50 65 70 75 80
53 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
54 85 90 95
57 Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
58 100 105 110
61 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
62 115 120 125
65 Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
66 130 135 140
69 Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
70 145 150 155 160
73 Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Val Leu Phe Met
74 165 170 175
77 Asn Asn Asn Thr Arg Leu Asn Trp Gln Asn Lys Asp Leu Asn Leu Phe

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78          180          185          190
81 Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
82          195          200          205
85 Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
86          210          215          220
89 Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
90 225          230          235          240
93 Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
94          245          250          255
97 Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
98          260          265          270
101 Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
102          275          280          285
105 Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
106          290          295          300
109 Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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114          325          330
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127 ttttggtgat tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc      180
129 agcatcagcc ggcttttctt gcatggactg ctgttcctga gtgctatcca gcttaccac      240
131 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg      300
133 attgcaaacc aagccaacct ctggcttget gctgacctca gctgcttta ctgctccaag      360
135 ctcatccgtt tctctcacac cttcctgatc tgcttgcaa gctgggtctc caggaagatc      420
137 tccagatgc tctgggtat tattcttgc tcctgcatct gcaactgtgc tttgtgttgg      480
139 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca      540
141 aggctcaact ggcagaataa agatctcaat ttattttatt cctttctctt ctgctatctg      600
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145 ggaaggcaca tgaggacaat gaaggtctat accagaaact ctcgtagacc cagcctggag      720
147 gccacatta aagccctcaa gtctcttctg tccttttctt gcttcttctg gatatcatcc      780
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151 gtttgtgttg ggataatggc agcttgtccc tctgggcagt cagccatcct gatctcaggc      900
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170          20          25          30
173 Leu Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly
174          35          40          45
177 Ile Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val
178          50          55          60
181 Gln Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser
182 65          70          75          80
185 Val Ser Arg Ile Ala Leu Gln Ser Leu Met Leu Glu Ile Thr Ile
186          85          90          95
189 Ser Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala
190          100          105          110
193 Phe Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala
194          115          120          125
197 Ala Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr
198          130          135          140
201 Pro Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp
202 145          150          155          160
205 Leu Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys
206          165          170          175
209 Ile Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser
210          180          185          190
213 Ser Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly
214          195          200          205
217 Leu Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe
218          210          215          220
221 Ile Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu
222 225          230          235          240
225 His Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala
226          245          250          255
229 His Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile
230          260          265          270
233 Phe Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile
234          275          280          285
237 Asn Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro
238          290          295          300
241 Ala Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg
242 305          310          315          320
245 Ala Trp Ser Gly Phe Ser Phe Asp Phe Ile Phe Thr Gln Lys Ser Gly
246          325          330          335
249 Leu
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254 <211> LENGTH: 1013
255 <212> TYPE: DNA
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261 ctctgcgatc ctgcagaaag tgaattgtcg ccatttctca tcaccttaat ttttagcagtt      120
263 ttacttgctg aatacctcat tggatcatt gcaaattggt tcatcatggc tatacatgca      180
265 gctgaatggg ttcaaaataa ggcagtttcc acaagtggca ggatcctggt tttcctgagt      240

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267 gtatccagaa tagctctcca aagcctcatg atggttagaaa ttaccatcag ctcaacctcc 300
269 ctaagttttt attctgaaga cgctgtatat tatgcattca aaataagttt tatattctta 360
271 aatttttgta gcctgtggtt tgctgcctgg ctacagtttct tctactttgt gaagattgcc 420
273 aattttctcct accccctttt cctcaaactg aggtggagaa ttactggatt gataccctgg 480
275 cttctgtggc tgtccgtggt tatttccttc agtcacagca tgttctgcat caacatctgc 540
277 actgtgtatt gtaacaattc tttccctatc cactcctcca actccactaa gaaaacatac 600
279 ttgtctgaga tcaatgtggt cggctctggct tttttcttta acctggggat tgtgactcct 660
281 ctgatcatgt tcatcctgac agccaccctg ctgatcctct ctctcaagag acacacccta 720
283 cacatgggaa gcaatgccac aggggtccaac gacccagca tggagggtca catggggggc 780
285 atcaaagcta tcagctactt tctcattctc tacattttca atgcagttgc tctgtttatc 840
287 tacctgtcca acatgtttga catcaacagt ctgtggaata atttgtgcca gatcatcatg 900
289 gctgcctacc ctgccagcca ctcaattcta ctgattcaag ataaccctgg gctgagaaga 960
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295 <211> LENGTH: 323
296 <212> TYPE: PRT
297 <213> ORGANISM: Homo sapiens
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305 Lys Val Thr Phe Thr Leu Val Val Ser Gly Ile Glu Cys Ile Thr Gly
306 20 25 30
309 Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
310 35 40 45
313 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
314 50 55 60
317 Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
318 65 70 75 80
321 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
322 85 90 95
325 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
326 100 105 110
329 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
330 115 120 125
333 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
334 130 135 140
337 Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu
338 145 150 155 160
341 Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
342 165 170 175
345 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
346 180 185 190
349 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
350 195 200 205
353 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
354 210 215 220
357 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
358 225 230 235 240
361 Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr

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362                               245                               250                               255
365 Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
366                               260                               265                               270
369 Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
370                               275                               280                               285
373 Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
374                               290                               295                               300
377 Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
378 305                               310                               315                               320
381 Gln Thr Leu
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386 <211> LENGTH: 969
387 <212> TYPE: DNA
388 <213> ORGANISM: Homo sapiens
390 <400> SEQUENCE: 6
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393 acttttggtg tctccggaat agagtgcac actggcatcc ttgggagtgg cttcatcacg      120
395 gccatctatg gggctgagtg ggccaggggc aaaacactcc ccactgggtga ccgcattatg      180
397 ttgatgctga gcttttccag gctcttgcta cagatttgga tgatgctgga gaacattttc      240
399 agtctgctat tccgaattgt ttataaccaa aactcagtg atatacctctt caaagtcac      300
401 actgtctttc tgaaccattc caatctctgg tttgctgcct ggctcaaagt cttctattgt      360
403 cttagaattg caaacttcaa tcataccttg ttcttctgta tgaagaggaa aatcatagtg      420
405 ctgatgcctt ggcttctcag gctgtcagtg ttggtttcct taagcttcag ctttctcttc      480
407 tgcagagatg tcttcaatgt gtatgtgaat agctccattc ctataccctc ctccaactcc      540
409 acggagaaga agtacttctc tgagaccaat atgggtcaacc tgggtatttt ctataacatg      600
411 gggatcttcg ttcctctgat catgttcac ctggcagcca ccctgctgat cctctctctc      660
413 aagagacaca ccctacacat gggaagcaat gccacagggg ccagggaacc cagcatgaag      720
415 gctcacatag gggccatcaa agccaccagc tactttctca tcctctacat tttcaatgca      780
417 attgctctat ttctttccac gtccaacatc tttgacactt acagttcctg gaatattttg      840
419 tgcaagatca tcatggctgc ctaccctgcc ggccactcag tacaactgat cttgggcaac      900
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427 <211> LENGTH: 307
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429 <213> ORGANISM: Homo sapiens
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438                               20                               25                               30
441 Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
442                               35                               40                               45
445 Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
446                               50                               55                               60
449 His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
450 65                               70                               75                               80
453 Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
454                               85                               90                               95

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:51,52

VERIFICATION SUMMARY

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